

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/777,144

Source: _____

Date Processed by STIC: _____

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/777,144

DATE: 10/18/2004

TIME: 09:18:43

Input Set : N:\Crf3\RULE60\10777144.raw.txt

Output Set: N:\CRF4\10182004\J777144.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Schlessinger, Joseph
6 Sap, Jan M.8 (ii) TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
9 PHOSPHATASE-ALPHA

11 (iii) NUMBER OF SEQUENCES: 14

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: PENNIE & EDMONDS
15 (B) STREET: 1155 AVENUE OF THE AMERICAS
16 (C) CITY: NEW YORK
17 (D) STATE: NEW YORK
18 (E) COUNTRY: U.S.A.
19 (F) ZIP: 10036

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/10/777,144
C--> 29 (B) FILING DATE: 13-Feb-2004

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

W--> 33 (A) APPLICATION NUMBER: US/09/280,597
34 (B) FILING DATE: 29-MARCH-1999

W--> 36 (A) APPLICATION NUMBER: US 08/015,985

37 (B) FILING DATE: 10-FEB-1993

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Coruzzi, Laura A.
41 (B) REGISTRATION NUMBER: 30,742
42 (C) REFERENCE/DOCKET NUMBER: 7683-020

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: (212) 790-9090
46 (B) TELEFAX: (212) 869-9741/8864
47 (C) TELEX: 66141 PENNIE

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 802 amino acids
55 (B) TYPE: amino acid
56 (D) TOPOLOGY: linear

58 (ii) MOLECULE TYPE: protein

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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62 Met Asp Ser Trp Phe Ile Leu Val Leu Leu Gly Ser Gly Leu Ile Cys
63 1 5 10 15
65 Val Ser Ala Asn Asn Ala Thr Thr Val Ala Pro Ser Val Gly Ile Thr
66 20 25 30
68 Arg Leu Ile Asn Ser Ser Thr Ala Glu Pro Val Lys Glu Glu Ala Lys
69 35 40 45
71 Thr Ser Asn Pro Thr Ser Ser Leu Thr Ser Leu Ser Val Ala Pro Thr
72 50 55 60
74 Phe Ser Pro Asn Ile Thr Leu Gly Pro Thr Tyr Leu Thr Thr Val Asn
75 65 70 75 80
77 Ser Ser Asp Ser Asp Asn Gly Thr Thr Arg Thr Ala Ser Thr Asn Ser
78 85 90 95
80 Ile Gly Ile Thr Ile Ser Pro Asn Gly Thr Trp Leu Pro Asp Asn Gln
81 100 105 110
83 Phe Thr Asp Ala Arg Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala
84 115 120 125
86 Ala Thr Thr Pro Glu Thr Phe Pro Pro Ser Gly Asn Ser Asp Ser Lys
87 130 135 140
89 Asp Arg Arg Asp Glu Thr Pro Ile Ile Ala Val Met Val Ala Leu Ser
90 145 150 155 160
92 Ser Leu Leu Val Ile Val Phe Ile Ile Ile Val Leu Tyr Met Leu Arg
93 165 170 175
95 Phe Lys Lys Tyr Lys Gln Ala Gly Ser His Ser Asn Ser Phe Arg Leu
96 180 185 190
98 Ser Asn Gly Arg Thr Glu Asp Val Glu Pro Gln Ser Val Pro Leu Leu
99 195 200 205
101 Ala Arg Ser Pro Ser Thr Asn Arg Lys Tyr Pro Pro Leu Pro Val Asp
102 210 215 220
104 Lys Leu Glu Glu Glu Ile Asn Arg Arg Met Ala Asp Asp Asn Lys Leu
105 225 230 235 240
107 Phe Arg Glu Glu Phe Asn Ala Leu Pro Ala Cys Pro Ile Gln Ala Thr
108 245 250 255
110 Cys Glu Ala Ala Ser Lys Glu Glu Asn Lys Glu Lys Asn Arg Tyr Val
111 260 265 270
113 Asn Ile Leu Pro Tyr Asp His Ser Arg Val His Leu Thr Pro Val Glu
114 275 280 285
116 Gly Val Pro Asp Ser Asp Tyr Ile Asn Ala Ser Phe Ile Asn Gly Tyr
117 290 295 300
119 Gln Glu Lys Asn Lys Phe Ile Ala Ala Gln Gly Pro Lys Glu Glu Thr
120 305 310 315 320
122 Val Asn Asp Phe Trp Arg Met Ile Trp Glu Gln Asn Thr Ala Thr Ile
123 325 330 335
125 Val Met Val Thr Asn Leu Lys Glu Arg Lys Glu Cys Lys Cys Ala Gln
126 340 345 350
128 Tyr Trp Pro Asp Gln Gly Cys Trp Thr Tyr Gly Asn Ile Arg Val Ser
129 355 360 365
131 Val Glu Asp Val Thr Val Leu Val Asp Tyr Thr Val Arg Lys Phe Cys
132 370 375 380
134 Ile Gln Gln Val Gly Asp Met Thr Asn Arg Lys Pro Gln Arg Leu Ile

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135	385	390	395	400
137	Thr Gln Phe His Phe Thr Ser Trp Pro Asp	Phe Gly Val Pro Phe Thr		
138	405	410	415	
140	Pro Ile Gly Met Leu Lys Phe Leu Lys Lys Val Lys Ala Cys Asn Pro			
141	420	425	430	
143	Gln Tyr Ala Gly Ala Ile Val Val His Cys Ser Ala Gly Val Gly Arg			
144	435	440	445	
146	Thr Gly Thr Phe Val Val Ile Asp Ala Met Leu Asp Met Met His Thr			
147	450	455	460	
149	Glu Arg Lys Val Asp Val Tyr Gly Phe Val Ser Arg Ile Arg Ala Gln			
150	465	470	475	480
152	Arg Cys Gln Met Val Gln Thr Asp Met Gln Tyr Val Phe Ile Tyr Gln			
153	485	490	495	
155	Ala Leu Leu Glu His Tyr Leu Tyr Gly Asp Thr Glu Leu Glu Val Thr			
156	500	505	510	
158	Ser Leu Glu Thr His Leu Gln Lys Ile Tyr Asn Lys Ile Pro Gly Thr			
159	515	520	525	
161	Ser Asn Asn Gly Leu Glu Glu Phe Lys Lys Leu Thr Ser Ile Lys			
162	530	535	540	
164	Ile Gln Asn Asp Lys Met Arg Thr Gly Asn Leu Pro Ala Asn Met Lys			
165	545	550	555	560
167	Lys Asn Arg Val Leu Gln Ile Ile Pro Tyr Glu Phe Asn Arg Val Ile			
168	565	570	575	
170	Ile Pro Val Lys Arg Gly Glu Glu Asn Thr Asp Tyr Val Asn Ala Ser			
171	580	585	590	
173	Phe Ile Asp Gly Tyr Arg Gln Lys Asp Ser Tyr Ile Ala Ser Gln Gly			
174	595	600	605	
176	Pro Leu Leu His Thr Ile Glu Asp Phe Trp Arg Met Ile Trp Glu Trp			
177	610	615	620	
179	Lys Ser Cys Ser Ile Val Met Leu Thr Glu Leu Glu Glu Arg Gly Gln			
180	625	630	635	640
182	Glu Lys Cys Ala Gln Tyr Trp Pro Ser Asp Gly Leu Val Ser Tyr Gly			
183	645	650	655	
185	Asp Ile Thr Val Glu Leu Lys Lys Glu Glu Glu Cys Glu Ser Tyr Thr			
186	660	665	670	
188	Val Arg Asp Leu Leu Val Thr Asn Thr Arg Glu Asn Lys Ser Arg Gln			
189	675	680	685	
191	Ile Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly Ile Pro Ser			
192	690	695	700	
194	Asp Gly Lys Gly Met Ile Ser Ile Ile Ala Ala Val Gln Lys Gln Gln			
195	705	710	715	720
197	Gln Gln Ser Gly Asn His Pro Ile Thr Val His Cys Ser Ala Gly Ala			
198	725	730	735	
200	Gly Arg Thr Gly Thr Phe Cys Ala Leu Ser Thr Val Leu Glu Arg Val			
201	740	745	750	
203	Lys Ala Glu Gly Ile Leu Asp Val Phe Gln Thr Val Lys Ser Leu Arg			
204	755	760	765	
206	Leu Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr Glu Phe Cys			
207	770	775	780	

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209 Tyr Lys Val Val Gln Glu Tyr Ile Asp Ala Phe Ser Asp Tyr Ala Asn
 210 785 790 795 800

212 Phe Lys

215 (2) INFORMATION FOR SEQ ID NO: 2:

217 (i) SEQUENCE CHARACTERISTICS:

218 (A) LENGTH: 2409 base pairs

219 (B) TYPE: nucleic acid

220 (C) STRANDEDNESS: double

221 (D) TOPOLOGY: unknown

223 (ii) MOLECULE TYPE: cDNA

225 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

227 ATGGATTCCCT	GGTCATTCT	TGTTCTGCTC	GGCAGTGGTC	TGATATGTGT	CAGTGCAAC	60
229 AATGCTACCA	CAGTTGCACC	TTCTGTAGGA	ATTACAAGAT	TAATTAACCT	ATCAACGGCA	120
231 GAACCAGTTA	AAGAAGAGGC	CAAAACTTCA	AATCCAACCTT	CTTCACTAAC	TTCTCTTCT	180
233 GTGGCACCAA	CATTCAAGCCC	AAATATAACT	CTGGGACCCA	CCTATTTAAC	CACTGTCAAT	240
235 TCTTCAGACT	CTGACAATGG	GACCACAAGA	ACAGCAAGCA	CCAATTCTAT	AGGCATTACA	300
237 ATTTCACCAA	ATGGAACGTG	GCTTCCAGAT	AACCAGTTCA	CGGATGCCAG	AACAGAACCC	360
239 TGGGAGGGGA	ATTCCAGCAC	CGCAGCAACC	ACTCCAGAAA	CTTTCCCTCC	TTCAGGTAAT	420
241 TCTGACTCGA	AGGACAGAAG	AGATGAGACA	CCAATTATTG	CGGTGATGGT	GGCCCTGTCC	480
243 TCTCTGCTAG	TGATCGTGT	TATTATCATA	GTGTTGTACA	TGTTAAGGTT	TAAGAAATAC	540
245 AAGCAAGCTG	GGAGCCATT	CAATTCTTC	CGCTTATCCA	ACGGCCGCAC	TGAGGATGTG	600
247 GAGCCCCAGA	GTGTGCCACT	TCTGGCCAGA	TCCCCAAGCA	CCAACAGGAA	ATACCCACCC	660
249 CTGCCCCGTG	ACAAGCTGGA	AGAGGAAATT	AACCGGAGAA	TGGCAGACGA	CAATAAGCTC	720
251 TTCAGGGAGG	AATTCAACGC	TCTCCCTGCA	TGTCCTATCC	AGGCCACCTG	TGAGGCTGCT	780
253 TCCAAGGAGG	AAAACAAGGA	AAAAAATCGA	TATGTAAACA	TCTTGCCTTA	TGACCACTCT	840
255 AGAGTCCACC	TGACACCGGT	TGAAGGGTT	CCAGATTCTG	ATTACATCAA	TGCTTCATT	900
257 ATCAACGGTT	ACCAAGAAAA	GAACAAATT	ATTGCTGCAC	AAGGACAAA	AGAAGAAACG	960
259 GTGAATGATT	TCTGGCGGAT	GATCTGGAA	CAAAACACAG	CCACCATCGT	CATGGTTACC	1020
261 AACCTGAAGG	AGAGAAAGGA	GTGCAAGTGC	GCCCCAGTACT	GGCCAGACCA	AGGCTGCTGG	1080
263 ACCTATGGGA	ATATTGGGT	GTCTGTAGAG	GATGTGACTG	TCCTGGTGG	CTACACAGTA	1140
265 CGGAAGTTCT	GCATCCAGCA	GGTGGGCGAC	ATGACCAACA	GAAAGCCACA	GCGCCTCATC	1200
267 ACTCAGTTCC	ACTTTACCA	CTGGCCAGAC	TTTGGGGTGC	CTTTTACCCC	GATGGCATG	1260
269 CTCAGTTCC	TCAAGAAGGT	GAAGGCTGT	AACCCCTCAGT	ATGCAGGGC	CATCGTGGTC	1320
271 CACTGCAGTG	CAGGTGTTAGG	GGGTACAGGT	ACCTTGTCG	TCATTGATGC	CATGCTGGAC	1380
273 ATGATGCATA	CAGAACGGAA	GGTGGACGTG	TATGGCTTTG	TGAGCCGGAT	CCGGGCACAG	1440
275 CGCTGCCAGA	TGGTGCAAAC	CGATATGCAG	TATGTCTTCA	TATACCAAGC	CCTTCTGGAG	1500
277 CATTATCTCT	ATGGAGATAC	AGAACTGGAA	GTGACCTCTC	TAGAAACCCA	CCTGCAGAAA	1560
279 ATTTACAACA	AAATCCCAGG	GACCAGCAAC	AATGGATTAG	AGGAGGGAGTT	TAAGAAGTTA	1620
281 ACATCAATCA	AAATCCAGAA	TGACAAGATG	CGGACTGGAA	ACCTTCCAGC	CAACATGAAG	1680
283 AAGAACCGTG	TTTTACAGAT	CATTCCATAT	GAATTCAACA	GAGTGATCAT	TCCAGTTAAC	1740
285 CGGGCGAAG	AGAATACAGA	CTATGTGAAC	GCATCCTTA	TTGATGGCTA	CCGGCAGAAG	1800
287 GACTCCTATA	TCGCCAGCCA	GGGCCCTCTT	CTCCACACAA	TTGAGGACTT	CTGGCGAATG	1860
289 ATCTGGGAGT	GGAAATCCTG	CTCTATCGTG	ATGCTAACAG	AACTGGAGGA	GAGAGGCCAG	1920
291 GAGAAGTGTG	CCCAGTACTG	GCCATCTGAT	GGACTGGTGT	CCTATGGAGA	TATTACAGTG	1980
293 GAACTGAAGA	AGGAGGAGGA	ATGTGAGAGC	TACACCGTCC	GAGACCTCCT	GGTCACCAAC	2040
295 ACCAGGGAGA	ATAAGAGCCG	GCAGATCCGG	CAGTTCCACT	TCCATGGCTG	GCCTGAAGTG	2100
297 GGATCCCCA	GTGACGGAAA	GGGCATGATC	AGCATCATCG	CCGCCGTGCA	GAAGCAGCAG	2160
299 CAGCAGTCAG	GGAACCACCC	CATCACCGTG	CACTGCAGCG	CCGGGGCAGG	AAGGACGGGG	2220
301 ACCTTCTGTG	CCCTGAGCAC	CGTCCTGGAG	CGTGTGAAAG	CAGAGGGGAT	TTTGGATGTC	2280

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303 TTCCAGACTG TCAAGAGCCT GCGGCTACAG AGGCCACACA TGGTCCAGAC ACTGGAACAG 2340
 305 TATGAGTTCT GCTACAAGGT GGTGCAGGAG TATATTGATG CATTCTCAGA TTATGCCAAC 2400
 307 TTCAAGTAA 2409
 310 (2) INFORMATION FOR SEQ ID NO: 3:
 312 (i) SEQUENCE CHARACTERISTICS:
 313 (A) LENGTH: 793 amino acids
 314 (B) TYPE: amino acid
 315 (D) TOPOLOGY: linear
 317 (ii) MOLECULE TYPE: protein
 319 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 321 Met Asp Ser Trp Phe Ile Leu Val Leu Phe Gly Ser Gly Leu Ile His
 322 1 5 10 15
 324 Val Ser Ala Asn Asn Ala Thr Thr Val Ser Pro Ser Leu Gly Thr Thr
 325 20 25 30
 327 Arg Leu Ile Lys Thr Ser Thr Thr Glu Leu Ala Lys Glu Glu Asn Lys
 328 35 40 45
 330 Thr Ser Asn Ser Thr Ser Ser Val Ile Ser Leu Ser Val Ala Pro Thr
 331 50 55 60
 333 Phe Ser Pro Asn Leu Thr Leu Glu Pro Thr Tyr Val Thr Thr Val Asn
 334 65 70 75 80
 336 Ser Ser His Ser Asp Asn Gly Thr Arg Arg Ala Ala Ser Thr Glu Ser
 337 85 90 95
 339 Gly Gly Thr Thr Ile Ser Pro Asn Gly Ser Trp Leu Ile Glu Asn Gln
 340 100 105 110
 342 Phe Thr Asp Ala Ile Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala
 343 115 120 125
 345 Ala Thr Thr Pro Glu Thr Phe Pro Pro Ala Asp Glu Thr Pro Ile Ile
 346 130 135 140
 348 Ala Val Met Val Ala Leu Ser Ser Leu Leu Val Ile Val Phe Ile Ile
 349 145 150 155 160
 351 Ile Val Leu Tyr Met Leu Arg Phe Lys Lys Tyr Lys Gln Ala Gly Ser
 352 165 170 175
 354 His Ser Asn Ser Phe Arg Leu Ser Asn Gly Arg Thr Glu Asp Val Glu
 355 180 185 190
 357 Pro Gln Ser Val Pro Leu Leu Ala Arg Ser Pro Ser Thr Asn Arg Lys
 358 195 200 205
 360 Tyr Pro Pro Leu Pro Val Asp Lys Leu Glu Glu Ile Asn Arg Arg
 361 210 215 220
 363 Met Ala Asp Asp Asn Lys Leu Phe Arg Glu Glu Phe Asn Ala Leu Pro
 364 225 230 235 240
 366 Ala Cys Pro Ile Gln Ala Thr Cys Glu Ala Ala Ser Lys Glu Glu Asn
 367 245 250 255
 369 Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser Arg
 370 260 265 270
 372 Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile Asn
 373 275 280 285
 375 Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala Ala
 376 290 295 300
 378 Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile Trp

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/18/2004
PATENT APPLICATION: US/10/777,144 TIME: 09:18:44

Input Set : N:\Crf3\RULE60\10777144.raw.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos.8,12,21,22,24,25,27,28,30,37,39,47,57,72,77,89,94,95,99,104
Seq#:9; Xaa Pos.109,111,115,116,124,125,131,133,135,137,138,139,143,144,153
Seq#:9; Xaa Pos.155,170,174,176,179,180,181,182,183,186,205,211,212,214,215
Seq#:9; Xaa Pos.217,222,227,230,232,240,244,247
Seq#:14; Xaa Pos.10,20,21,22,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38
Seq#:14; Xaa Pos.39,40,41,42,43,55,67,70,87,95,96,97,99,100,103,105,106,112
Seq#:14; Xaa Pos.114,115,116,120,121,123,126,127,128,133,137,138,139,141
Seq#:14; Xaa Pos.143,149,151,182,186,188,195,196,197,198,199,200,201,202
Seq#:14; Xaa Pos.205,209,212,213,214,218,222,224,228,229,244,247,254,257
Seq#:14; Xaa Pos.264,265,266,267

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10777144.raw.txt
Output Set: N:\CRF4\10182004\J777144.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:36 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:837 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
M:341 Repeated in SeqNo=9
L:1143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
M:341 Repeated in SeqNo=14